

配列表

<110> SAITO, Koichi

<120> Estrogen receptor genes and uses thereof

<130> 561334

<150> JP 2002-004395

<151> 2002-01-11

<160> 48

<210> 1

<211> 506

<212> PRT

<213> Blue Gill

<400> 1

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20 25 30

Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu

35	40	45
Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe		
50	55	60
Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp		
65	70	75
Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His		
85	90	95
Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn		
100	105	110
Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val		
115	120	125
Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg		
130	135	140
Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys		
145	150	155
Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser		
165	170	175
Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly		
180	185	190
Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro		
195	200	205
Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr		
210	215	220
Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met		

225	230	235	240
Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His			
	245	250	255
Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile			
	260	265	270
Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala			
	275	280	285
Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe			
	290	295	300
Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met			
305	310	315	320
Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu			
	325	330	335
Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu			
	340	345	350
His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala			
	355	360	365
Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser			
	370	375	380
Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met			
385	390	395	400
Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys			
	405	410	415
Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile			

420 425 430
 His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu
 435 440 445
 Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly
 450 455 460
 Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His
 465 470 475 480
 Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly
 485 490 495
 Gly Ser Arg Ser Asp Cys Thr His Ile Leu
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<211> 3499

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (424)... (1944)

<400> 2

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ccctctcagt gacatgtacc ctgaagagag caggggggtcc ggaggggtag ccactgtgga	180
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ccagtctggc tactactctg tacctctgga cgcccaaggg ccaccctcag atggcagcct	300
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cagccccctt atgcaccgc ccagccacca ctatctggaa accacctcaa caccgtcta	420
cag atg agt ctg aaa gac tgg tta tta gga aaa gaa agg acg gtg gtg	468
Met Ser Leu Lys Asp Trp Leu Leu Gly Lys Glu Arg Thr Val Val	
1 5 10 15	
acc atg gag gag ctg agg tct agt gtc cca tcc agc cag cag cca gtt	516
Thr Met Glu Glu Leu Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val	
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ccc aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg	564
Pro Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly	
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gag tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt	612
Glu Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg	
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ttc tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg	660
Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val	
65 70 75	
tgg tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt	708
Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly	
80 85 90 95	
cac aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg	756

His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg	
100 105 110	
aat cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa	804
Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu	
115 120 125	
gtg ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg	852
Val Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu	
130 135 140	
cgc cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct	900
Arg Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser	
145 150 155	
aag gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac	948
Lys Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His	
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agc agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc	996
Ser Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr	
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ggg atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc	1044
Gly Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro	
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cca atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc	1092
Pro Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val	
210 215 220	
acc ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac	1140

Thr Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His	
225 230 235	
atg atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc	1188
Met Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu	
240 245 250 255	
cat gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg	1236
His Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met	
260 265 270	
att ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc	1284
Ile Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe	
275 280 285	
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Ala Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly	
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Phe Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg	
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atg ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc	1428
Met Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile	
320 325 330 335	
ctg ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc	1476
Leu Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro	
340 345 350	
ctc cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac	1524

Leu His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp
 355 360 365
 gct ctc ata cat cat atc agc caa tca gga tgc tcg gct cag cag cag 1572
 Ala Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln
 370 375 380
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 Ser Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His
 385 390 395
 atg agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac 1668
 Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn
 400 405 410 415
 aaa gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt 1716
 Lys Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg
 420 425 430
 ata cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga 1764
 Ile His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly
 435 440 445
 gag cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat 1812
 Glu Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn
 450 455 460
 ggc ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac 1860
 Gly Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn
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 cac gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac 1908

His	Glu	Ser	Pro	Ser	Arg	Gly	Pro	Thr	Gly	Pro	Gly	Val	Leu	Gln	Tyr	
480					485					490					495	
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Gly Gly Ser Arg Ser Asp Cys Thr His Ile Leu																
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<210> 3

<211> 996

<212> DNA

<213> Blue Gill

<400> 3

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atgaaaggag gtgttcgcaa ggaccgtggc cgtgttttgc gccgtgataa acgacgtgct 180
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tgctcccgtc agaagctgag ccgaccgtac accgaggtca ccataatgac actactcacc 420
agcatggccg ataaggagct ggtccacatg atcacctggg ccaagaagct tccaggtttc 480
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<213> Blue Gill

65 70 75 80

His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser Thr Pro Val Tyr
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100 105 110

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115 120 125

Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe Cys Ala Val Cys
130 135 140

Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
145 150 155 160

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
165 170 175

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn Arg Arg Lys Ser
180 185 190

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
195 200 205

Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg Arg Asp Lys Arg
210 215 220

Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys Asp Leu Glu Tyr
225 230 235 240

Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser Ser Ser Ser Ser
245 250 255

Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly Met Ser Pro Asp
260 265 270

Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro Met Leu Cys Ser
275 280 285

Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr Ile Met Thr Leu
290 295 300

Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met Ile Thr Trp Ala
305 310 315 320

Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His Asp Gln Val Gln
325 330 335

Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile Gly Leu Ile Trp
340 345 350

Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala Gln Asp Leu Ile
355 360 365

Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe Val Glu Ile Phe
370 375 380

Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met Leu Lys Leu Lys
385 390 395 400

Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly
405 410 415

Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Met
420 425 430

Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His His
435 440 445

Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser Arg Arg Gln Ala
450 455 460

Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly
 465 470 475 480
 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr
 485 490 495
 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile His Arg Pro Asp
 500 505 510
 Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu Pro Pro Phe Ile
 515 520 525
 Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly Gly Val Ser Ser
 530 535 540
 Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His Glu Ser Pro Ser
 545 550 555 560
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 565 570 575
 Asp Cys Thr His Ile Leu
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<210> 5

<211> 1824

<212> DNA

<213> Blue Gill

<220>

<221> CDS

<222> (74)... (1822)

<400> 5

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Met Tyr Pro Glu Glu Ser Arg Gly Ser Gly Gly Val	
1 5 10	
gcc act gtg gac ttt ctg gaa ggg acc tac gat tat gcc gcc ccc acc	157
Ala Thr Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr Ala Ala Pro Thr	
15 20 25	
cct gcc ccg act cct ctt tac agc cag tct ggc tac tac tct gta cct	205
Pro Ala Pro Thr Pro Leu Tyr Ser Gln Ser Gly Tyr Tyr Ser Val Pro	
30 35 40	
ctg gac gcc caa ggg cca ccc tca gat ggc agc ctt cag tcc ctg ggc	253
Leu Asp Ala Gln Gly Pro Pro Ser Asp Gly Ser Leu Gln Ser Leu Gly	
45 50 55 60	
agc ggg cct acc agt cct ctt gtg ttt gtg ccg tcc agc ccc aga ctc	301
Ser Gly Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu	
65 70 75	
agc ccc ttt atg cac ccg ccc agc cac cac tat ctg gaa acc acc tca	349
Ser Pro Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser	
80 85 90	
aca ccc gtc tac agg tct agt gtc cca tcc agc cag cag cca gtt ccc	397
Thr Pro Val Tyr Arg Ser Ser Val Pro Ser Ser Gln Gln Pro Val Pro	

95	100	105	
aga gag gac cag tgt gcc acc agt gat gag tcc tat agt gtg ggg gag			445
Arg Glu Asp Gln Cys Ala Thr Ser Asp Glu Ser Tyr Ser Val Gly Glu			
110	115	120	
tca ggg gct gga gcc agg ggg ttt gag atg gcc aag gag atg cgt ttc			493
Ser Gly Ala Gly Ala Arg Gly Phe Glu Met Ala Lys Glu Met Arg Phe			
125	130	135	140
tgt gct gtg tgc agt gac tat gcc tct ggg tac cac tac ggg gtg tgg			541
Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp			
145	150	155	
tcc tgt gaa ggc tgt aag gcc ttc ttt aag agg agc atc cag ggt cac			589
Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His			
160	165	170	
aat gac tat atg tgc cca gca acc aat cag tgt act att gac agg aat			637
Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn			
175	180	185	
cgg aga aag agc tgc cag gct tgc cgt ctt agg aag tgt tat gaa gtg			685
Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val			
190	195	200	
ggc atg atg aaa gga ggt gtt cgc aag gac cgt ggc cgt gtt ttg cgc			733
Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Gly Arg Val Leu Arg			
205	210	215	220
cgt gat aaa cga cgt gct gga acc aat gac cga gag aag gcc tct aag			781
Arg Asp Lys Arg Arg Ala Gly Thr Asn Asp Arg Glu Lys Ala Ser Lys			

225	230	235	
gac ctg gag tac aaa aca gtg ccc cct cag gac agg agg aaa cac agc			829
Asp Leu Glu Tyr Lys Thr Val Pro Pro Gln Asp Arg Arg Lys His Ser			
240	245	250	
agc agc agc agt gcc ggt ggt gga gga gga aaa tca tca gtg acc ggg			877
Ser Ser Ser Ser Ala Gly Gly Gly Gly Gly Lys Ser Ser Val Thr Gly			
255	260	265	
atg tct cct gac cag gtg ctc ctc ctg ctc cag ggt gcc gag ccc cca			925
Met Ser Pro Asp Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro			
270	275	280	
atg ctg tgc tcc cgt cag aag ctg agc cga ccg tac acc gag gtc acc			973
Met Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr			
285	290	295	300
ata atg aca cta ctc acc agc atg gcc gat aag gag ctg gtc cac atg			1021
Ile Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met			
305	310	315	
atc acc tgg gcc aag aag ctt cca ggt ttc ctg cag ctg tct ctc cat			1069
Ile Thr Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His			
320	325	330	
gac cag gtg cag ctg ctg gag agc tcg tgg ctg gag gtg ctg atg att			1117
Asp Gln Val Gln Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile			
335	340	345	
ggg ctc ata tgg agg tcc atc cac tgc ccc ggc aaa ctc atc ttc gca			1165
Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala			

350	355	360	
cag gac ctc ata ctg gac agg aat gaa ggt gac tgt gtg gaa ggc ttt			1213
Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Phe			
365	370	375	380
gtt gag atc ttc gac atg ctg ctg gcc act gcc tcc cgc ttc cgc atg			1261
Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Met			
385	390	395	
ctc aaa ctc aaa cct gag gag ttt gtc tgc ctc aaa gct atc atc ctg			1309
Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu			
400	405	410	
ctc aac tct ggt gcc ttc tct ttc tgc acc ggc aca atg gag ccc ctc			1357
Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu			
415	420	425	
cac aac agc atg gca gtg cag aac atg ctg gac acc atc aca gac gct			1405
His Asn Ser Met Ala Val Gln Asn Met Leu Asp Thr Ile Thr Asp Ala			
430	435	440	
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Leu Ile His His Ile Ser Gln Ser Gly Cys Ser Ala Gln Gln Gln Ser			
445	450	455	460
agg cgg cag gcc cag ctg ctg ctc ctg ctc tcc cac atc agg cac atg			1501
Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met			
465	470	475	
agc aac aaa ggc atg gag cat ctc tac agc atg aag tgc aag aac aaa			1549
Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys			

480	485	490	
gtg cct ctt tac gac ctt ctg ctg gag atg ttg gac gct cac cgt ata			1597
Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Ile			
495	500	505	
cac cgc cca gac aga cca gct cag ttc tgg tcc cag gct gac gga gag			1645
His Arg Pro Asp Arg Pro Ala Gln Phe Trp Ser Gln Ala Asp Gly Glu			
510	515	520	
cct ccc ttc att aac aac aac aac agc agc aac agt ggc agc aat ggc			1693
Pro Pro Phe Ile Asn Asn Asn Asn Ser Ser Asn Ser Gly Ser Asn Gly			
525	530	535	540
ggc gtc tcc tct tca gtc ggt tcc agt tca gga ccc cga gtc aac cac			1741
Gly Val Ser Ser Ser Val Gly Ser Ser Ser Gly Pro Arg Val Asn His			
545	550	555	
gag agc ccg agc aga gga ccc aca ggt cca gga gtc ctg cag tac gga			1789
Glu Ser Pro Ser Arg Gly Pro Thr Gly Pro Gly Val Leu Gln Tyr Gly			
560	565	570	
ggg tcc cgc tct gac tgc acc cac atc cta tga gg			1824
Gly Ser Arg Ser Asp Cys Thr His Ile Leu			
575	580		

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 6

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<212> PRT

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5

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15

Val Asp Ser Ser Arg Val Gly Ser Arg Val Val Ser Pro Ile Leu Asn

20

25

30

Ser	Pro	Leu	Glu	Arg	Ser	Gln	Pro	Ile	Cys	Ile	Pro	Ser	Pro	Tyr	Thr
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	50						55						60		
Phe	Ser	Tyr	Ala	Ser	Pro	Gly	Ile	Ser	Asp	Cys	Pro	Ser	Val	His	Gln
	65						70						75		80
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							85						90		95
Pro	Ile	Pro	Leu	His	His	Ser	Gln	Pro	Arg	Pro	Gln	His	Arg	Gln	Pro
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Ile	Gln	Ser	Pro	Trp	Val	Glu	Leu	Ser	Pro	Leu	Glu	Ser	Thr	Leu	Thr
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Thr	Ser	Lys	Ser	Val	Arg	Arg	Arg	Ser	Gln	Glu	Ser	Glu	Asp	Gly	Val
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									165					170	175
Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Arg	His	Asn	Asp	Tyr	Ile	Cys
									180					185	190
Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys
									195					200	205
Gln	Ala	Cys	Arg	Leu	Arg	Lys	Cys	Asn	Glu	Val	Gly	Met	Thr	Lys	Cys
									210					215	220

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225 230 235 240
Val Thr Arg Leu Ser Thr Gln Gly Arg Thr Asn Arg Thr Ala Val Leu
245 250 255
Thr Gly Pro Ala Val Gly Ser Leu Ile Ser Leu Asn Ser Pro Ala Leu
260 265 270
Thr Pro Glu Gln Leu Ile Glu Arg Ile Ile Asp Ala Glu Pro Pro Glu
275 280 285
Ile Tyr Leu Met Lys Asp Met Arg Arg Pro Leu Thr Glu Ala Asn Val
290 295 300
Met Met Ser Leu Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile
305 310 315 320
Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp
325 330 335
Gln Val His Leu Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly
340 345 350
Leu Met Trp Arg Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg
355 360 365
Asp Leu Ser Leu Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala
370 375 380
Glu Ile Phe Asp Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu
385 390 395 400
Lys Leu Gln Arg Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu
405 410 415

Asn Ser Asn Met Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln
420 425 430
Ser Arg Ser Lys Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu
435 440 445
Val Trp Ala Ile Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr
450 455 460
Arg Leu Ala His Leu Leu Met Leu Leu Ser His Ile Arg His Val Ser
465 470 475 480
Asn Lys Gly Met Asp His Leu His Cys Met Lys Met Lys Asn Met Val
485 490 495
Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala His Ile Met His
500 505 510
Ser Ser Arg Leu Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln
515 520 525
Arg Glu Ala Pro Ala Arg Pro His Ser Cys Gly Ser Gly Pro Leu Asn
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Met Ala Cys Ser

1

cca gag aag gat cag ccc ctc ctc cag ctc cag aag gtg gac tcc agt 165
Pro Glu Lys Asp Gln Pro Leu Leu Gln Leu Gln Lys Val Asp Ser Ser

5 10 15 20

cga gtt ggc agt cgt gtc gtc tcc ccg atc ctc aac tcc ccg ttg gaa 213
Arg Val Gly Ser Arg Val Val Ser Pro Ile Leu Asn Ser Pro Leu Glu

25 30 35

aga agc cag ccc atc tgc atc ccc tcc cct tac acc gac ctc agc cac 261
Arg Ser Gln Pro Ile Cys Ile Pro Ser Pro Tyr Thr Asp Leu Ser His

40 45 50

gac ttc acc acc ata cct ttc tac agt cca act ttc ttt agt tat gcc 309
Asp Phe Thr Thr Ile Pro Phe Tyr Ser Pro Thr Phe Phe Ser Tyr Ala

55 60 65

agt cca ggc att tca gac tgc ccc tcc gtc cat cag tca cta agc ccc 357
Ser Pro Gly Ile Ser Asp Cys Pro Ser Val His Gln Ser Leu Ser Pro

70 75 80

tcc tta ttc tgg ccc agc cat ggc cat gtt ggg tcc ccc ata ccc ctg 405

Ser Leu Phe Trp Pro Ser His Gly His Val Gly Ser Pro Ile Pro Leu

85 90 95 100

cac cac tcc cag cct cga cct cag cac aga cag cca atc cag agt cca 453

His His Ser Gln Pro Arg Pro Gln His Arg Gln Pro Ile Gln Ser Pro

105 110 115

tgg gtg gag ttg tca cca ctg gag agc acc tta aca acc agt aag agt 501

Trp Val Glu Leu Ser Pro Leu Glu Ser Thr Leu Thr Thr Ser Lys Ser

120 125 130

gta agg agg cgt tct cag gag agc gag gat ggc gtg gtg tcg tcc ggc 549

Val Arg Arg Arg Ser Gln Glu Ser Glu Asp Gly Val Val Ser Ser Gly

135 140 145

ggg aag gcg gac atc cac tac tgc gct gtg tgt cac gac tac gcc tca 597

Gly Lys Ala Asp Ile His Tyr Cys Ala Val Cys His Asp Tyr Ala Ser

150 155 160

gga tac cac tac ggc gtc tgg tca tgt gag ggg tgt aag gcc ttc ttc 645

Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe

165 170 175 180

aag agg agc atc caa aga cac aat gac tac atc tgc cca gca acc aat 693

Lys Arg Ser Ile Gln Arg His Asn Asp Tyr Ile Cys Pro Ala Thr Asn

185 190 195

caa tgc act ata gac aag aac cgc cgt aag agc tgc cag gcg tgc cgc 741

Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg

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Leu Arg Lys Cys Asn Glu Val Gly Met Thr Lys Cys Gly Val Arg Lys			
215	220	225	
gag cgt ggg aac tgc aga aac ccc cag atg agg cga gtg acc cga ctc			837
Glu Arg Gly Asn Cys Arg Asn Pro Gln Met Arg Arg Val Thr Arg Leu			
230	235	240	
tcc aca cag ggc aga act aac aga aca gct gtg tta act gga cca gcc			885
Ser Thr Gln Gly Arg Thr Asn Arg Thr Ala Val Leu Thr Gly Pro Ala			
245	250	255	260
gtg ggt tca cta atc tcg ctc aac tct cct gca ctg acc cca gag cag			933
Val Gly Ser Leu Ile Ser Leu Asn Ser Pro Ala Leu Thr Pro Glu Gln			
265	270	275	
ctg att gaa cga ata att gat gct gag cca cca gag atc tac ctc atg			981
Leu Ile Glu Arg Ile Ile Asp Ala Glu Pro Pro Glu Ile Tyr Leu Met			
280	285	290	
aaa gac atg agg agg cct ctg act gaa gca aac gtc atg atg tcg ctc			1029
Lys Asp Met Arg Arg Pro Leu Thr Glu Ala Asn Val Met Met Ser Leu			
295	300	305	
aca aac ctt gct gat aag gag ctg gtt cac atg atc agc tgg gcc aag			1077
Thr Asn Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys			
310	315	320	
aag att cca ggg ttt gta gag ctc agt ctc ttg gac cag gtg cac ctg			1125
Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Leu Asp Gln Val His Leu			

325	330	335	340	
ttg gag tgc tgc tgg ctg gag gtg ctg atg gtt gga ctg atg tgg agg				1173
Leu Glu Cys Cys Trp Leu Glu Val Leu Met Val Gly Leu Met Trp Arg				
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tca gtg gac cat cct ggg aaa ctt atc ttc tcc cgg gac ctc agc ctg				1221
Ser Val Asp His Pro Gly Lys Leu Ile Phe Ser Arg Asp Leu Ser Leu				
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agc aga gaa gag ggg agc tgt gtc cag ggc ttc gca gag atc ttt gat				1269
Ser Arg Glu Glu Gly Ser Cys Val Gln Gly Phe Ala Glu Ile Phe Asp				
	375	380	385	
atg ctg ata gct gcc acg tcc agg gtg aga gag ctc aag ctc cag agg				1317
Met Leu Ile Ala Ala Thr Ser Arg Val Arg Glu Leu Lys Leu Gln Arg				
	390	395	400	
gag gag tac gtc tgc ctc aag gcc atg atc ctc ctt aac tcc aac atg				1365
Glu Glu Tyr Val Cys Leu Lys Ala Met Ile Leu Leu Asn Ser Asn Met				
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tgc ctc ggc tcc tca gag ggc agc gag gag ctg cag agt cgc tcc aag				1413
Cys Leu Gly Ser Ser Glu Gly Ser Glu Glu Leu Gln Ser Arg Ser Lys				
	425	430	435	
ctg ctg tgt ctt ctg gac gct gta acg gac gct ctg gtg tgg gcc atc				1461
Leu Leu Cys Leu Leu Asp Ala Val Thr Asp Ala Leu Val Trp Ala Ile				
	440	445	450	
gcc aaa act ggc ctc act ttc cgc caa cag tac acc cgc ctc gcc cac				1509
Ala Lys Thr Gly Leu Thr Phe Arg Gln Gln Tyr Thr Arg Leu Ala His				

455 460 465
ctg ctt atg ctg ctc tca cac atc cgc cat gtc agt aac aaa ggc atg 1557
Leu Leu Met Leu Leu Ser His Ile Arg His Val Ser Asn Lys Gly Met
470 475 480
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Asp His Leu His Cys Met Lys Met Lys Asn Met Val Pro Leu Tyr Asp
485 490 495 500
ctg ctg ctg gag atg ttg gat gcc cac atc atg cac agc tcc cgt ctg 1653
Leu Leu Leu Glu Met Leu Asp Ala His Ile MET His Ser Ser Arg Leu
505 510 515
tct cac cag ccc ata cag caa gac gca cag gac cag agg gag gct cct 1701
Ser His Gln Pro Ile Gln Gln Asp Ala Gln Asp Gln Arg Glu Ala Pro
520 525 530
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963

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494

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Blue gill

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gagaaggatc agccccctcc

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